

MDK1'-T1

2002	2092
V A V A G T Î I L V P M V P G P I I G R R H C G Y S K A D Q GTGGCTGTAGCAGGACCATCATCTTGGTGTTCATGGTGTTCATCATTGGAAGAAGGCACTGTGGTTATAGCAAGACGCTGACCAA 600	EGDEELYPHSCTOTTOTTTAGTAACAATGAGCACCTGTCAGTTTATAAACCGCAACAATGAGCAAC

silves (appl

	2182 2272 2362 2452 2542 2632 2722 2812 2901
1	regetal grectga reartge lataaag atttga attect feratta
)	cttatttr aastacati gaatttro grattro ittgttto ttataaaco tacaaco
	acattotgo acatatat ttatagtgi ttgtaatt ittgtaatt acatttgta acatatet
	coctttate geagigit tttaaagg ttaaaatg ttataaagg tataagg
	tcccatttt taaaggct taaaggct agatttgg tttaactt tctaattt tctaattt igtgatagc
	ttttaag aaaattaag aaatgaacg tgaaaca tgaaact eggaectt tgatattt
	aatcaaga gtgatacc gctttgtt cttgaacc tgggtgca tattacct tattccct
	gcagaata gattgaat gtttggtg atctttgt catgetcc cetectcc cettttgaa
	caactaca ctgatctt gaaagatt gcctacct gttacctg actggcta cttggtca aactatgt
	taaacaat atttaact Ccaaatat Gcaagcat Gggcat Ctgtcata Gtggttag
	caattttggataaacaatcaactacagcagaataaatcaagatttttaagtcccattttcctttatacattctggttattttgtgttat atgtttattttttaaactctgatcttgattgatgtgataccataagcacagttaggctgcagtgtaaatatataaagacattgtctga gagcagtacgatttcatggaaagattgtttggtggctttgttaaaattaataaagaatttttaaggatatagtgatatttccattgc attaatataaaccaaatatgcctacctatctttgtctgaaccaaatgaatagatttgaaatgatactttatggaatatgtaattgaatttga ttgactgagcattatgtgttacctgcatgcttctgggtgcattgaaatatttcaaatgataatgaaaagtttata ctacctttgtgaggcatactggtcaccgctactattagctaagatcttccaaagccttataatgaaaaggttatatata
	T C T C T B G E E

MDK1-T2

2002 2092 2182 2272 V A V A G T I I L V P M V P G P.I.I G R R H C G Y S K A D Q GTGGCTGTAGCAGGGACCATCATCTTGGTGTTCGGCTTCATCATTGGAAGAAGGCACTGTGGTTATAGCAAGGCTGACCAA GCATCGTGCTCTCGTTTGTAGgtctcttttcctaatcaacactatgattttgaagtacgcgtacacgaagcaaacggaagaagaaga 610 570 900 SR ပ A S

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		. MDK1. . MDK1.Δ1 . MDK1.Δ2 . MDK1.T1
	MDK1-∆1 MDK1-∆2 MDK1-T1 MDK1-T1 MDK1-T2	DPNRAVHQPAKE DPNRAVHQPAKE DPNRAVHQPAKE
alternative 3'UTR		LEEASGKAPEATAVSSEQNPVIIIAVVAVAGTIILVPRVPGPIIGRRHCGYSKADQEGDEELYPHPKPPGTKTYIDPETYEDPNRAVHQPAKE. LEEASATAVSSEQNPVIIIAVVAVAGTIILVPRVPGPIIGRRHCGYSKADQEGDEELYPHPKPPGTKTYIDPETYEDPNRAVHQPAKE. LEEASGKAPEATAVSSEQNPVIIIAVVAVAGTIILVPRVPGPIIGRRHCGYSKADQEGDEELYPHSLYTHEHLSVL LEEASGKAPEATAVSSEQNPVIIIAVVAVAGTIILVPRVPGPIIGRRHCGYSKADQEGDEELYPHSLVTNEHLSVL LEEASGKAPEATAVSSEQNPVIIIAVVAVAGTIILVPRVPGPIIGRRHCGYSKADQEGDEELYPHSLYTHERGDGKEKTQHDKKWHIASCSRL
3'UTR		LEEASGKAPEATAVSSEQNPVIIIAVVAVAGTIILVPHVPGPIIGRRHCGYSKADQEGDEELYPHPKPPGTKTYID LEEASATAVSSEQNPVIIIAVVAVAGTIILVPHVPGPIIGRRHCGYSKADQEGDEELYPHPKPPGTKTYID LEEASGKAPEATAVSSEQNPVIIIAVVAVAGTIILVPHVPGPIIGRRHCGYSKADQEGDEELYPHSLVTNEHLSVL LEEASGKAPEATAVSSEQNPVIIIAVVAVAGTIILVPHVPGPIIGRRHCGYSKADQEGDEELYPHSLVTNEHLSVL
Kinase Domain		VPGP I I GRRHCGY. VPGP I I GRRHCGY. VPGP I I GRRHCGY!
Σ E		TIILVPM FIILVPM FIILVPM
Extracellular Domain		ONPVIIIAVVAVAG QNPVIIIAVVAVAG QNPVIIIAVVAVAGI
5'UTR		(PEATAVSSE)ATAVSSE IPEATAVSSE IPEATAVSSE
		LEEASGKY LEEASGKY LEEASGKY